

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ullrich, Axel
Aoki, Naohito
Kim, Yeong Woong
Wang, Hong Yang
Chen, Zhengjun
Naylor, Oliver
Kharitononkov, Alexei Igorevich
- (ii) TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
AND SIRP POLYPEPTIDES AND RELATED
PRODUCTS AND METHODS
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
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Suite 4700
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(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/877,150
(B) FILING DATE: June 17, 1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: U.S. 60/019,629
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- (A) APPLICATION NUMBER: U.S. 60/023,485
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- (A) APPLICATION NUMBER: U.S. 60/030,860
(B) FILING DATE: November 13, 1996

- (A) APPLICATION NUMBER: U.S. 60/034,286
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- (A) APPLICATION NUMBER: U.S. 60/030,964
(B) FILING DATE: November 15, 1996

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 225/298

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: "Xaa" in positions 3 and 5 stands
for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Phe Trp Xaa Met Xaa Trp
1 5

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: "Xaa" in position 6 stands for
either Ser, Ile or Val.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

His Cys Ser Ala Gly Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Phe Leu Glu Arg Leu Glu
1 5

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: "Xaa" in positions 3 and 5 stands for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Arg Trp Xaa Met Xaa Trp
1 5

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 6 stands for either Ser, Ile or Val.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

His Cys Ser Ala Gly Xaa Gly
 1 5

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTCTGTGTCC ACAGCAGTGC TGGCTGT

27

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

His Arg Asp Leu Ala Ala Arg
 1 5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in position 2 stands for Val or Met. "Xaa" in position 5 stands for Tyr or Phe.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp Xaa Trp Ser Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CGGGATCCCT TCGCCTTGCA GCTTTGTC

28

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CGGAATTCCT AGACTGATAC AGTCTGTAAG

30

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Asp Leu Lys Pro Glu Asn
1 5

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Ala Met Met Glu Arg Ile
1 5

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TATAGCGGCC GCTAGACTGA TACAGTCTGT

30

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TCCCCCGGGA TGCCCCATCC CCGAAGGTAC CA

32

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TATAGCGGCC GCTCACCGAC TGATATCCCG ACTGGAGTC

39

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TCCCCCGGGG AGACGATGCA TCACTGTAAG

30

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TATAGCGGCC GCGCTGGCCT GCACCTGTCA TCTGCTGGG

39

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CGGAATTCAT GCGGCATTCC AAACGAACTC

30

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TATAGCGGCC GCCCTGACTC CCACTCATTT CCTTTTAA

39

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CGGAATTCCG CCACCATGGC CCCTATACTA GGTAT

36

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GCCAAGCTTG CCACCATGGC CCCTATACTA GGTAT

36

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTAGCAGTAA GAATAGTTAA A

21

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GTTGCCCTGA GGATCATTAA GAAT

24

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GTTGCCCTGA GGATCATCCG GAAT

24

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

TACAATTCTC ACTGCTACAT GTAAGCCATC

30

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Pro Ile Tyr Ser Phe Ile Gly Gly Glu His Phe Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ile Val Glu Pro Asp Thr Glu Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Tyr Gly Phe Ser Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Ile Lys Glu Val Ala His Val Asn Leu Glu Val Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Val Ala Ala Gly Asp Ser Ala Thr
1 5

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GAATTCCGGC	ACGAGGCGGG	TTGCAGTATG	AGTCGCCAAT	CGGACCTAGT	GAGGAGCTTC	60
TTGGAGCAGC	AGGAGGCCCC	GGACCACCGG	AAGGGGGCAA	TCCTCGCCCC	TGAGTTCAGC	120
GACATTAAGG	CCCGCTCAGT	GGCTTGGAAG	ACTGAAGGTG	TGTGCTCCAC	TAAAGCCGGC	180
AGTCAGCAGG	GAAACTCAAA	GAAGAACCGC	TACAAAGACG	TGGTACCGTA	TGATGAGACG	240
AGAGTCATCC	TTTCCCTGCT	CCAGGAGGAA	GGACACGGAG	ATTACATTAA	TGCCAACTTC	300
ATCCGGGGCA	CAGATGGAAG	CCAGGCCTAC	ATTGCGACGC	AAGGACCCCT	GCCTCACACT	360
CTGTTGGACT	TCTGGCGCCT	GGTTTGGGAG	TTTGGAATCA	AGGTGATCTT	GATGGCCTGT	420
CAGGAGACAG	AAAATGGACG	GAGGAAGTGT	GAACGCTACT	GGGCCCAGGA	GCGGGAGCCT	480
CTACAGGCCG	GGCCTTTCTG	CATCACCTTG	ACAAAGGAGA	CAGCACTGAC	TTCGGACATC	540
ACTCTCAGGA	CCCTCCAGGT	TACATTCCAG	AAGGAATCCC	GTCTGTGCA	CCAGCTACAG	600
TACATGTCTT	GGCCGGACCA	CGGGGTTCCT	AGCAGTTCCG	ATCACATTCT	CACCATGGTG	660
GAGGAGGCC	GTTGCCTCCA	AGGACTTGGA	CCTGGACCCC	TCTGTGTCCA	CTGCAGTGCT	720
GGCTGTGGAC	GAACAGGTGT	CTTGTGTGCT	GTTGATTACG	TGAGGCAGTT	GCTTCTGACT	780
CAGACAATCC	CACCCAATTT	CAGCCTCTTT	GAAGTGGTCC	TGGAGATGCG	GAAACAGCGA	840
CCTGCAGCGG	TGCAGACAGA	GGAGCAGTAC	AGGTTCTCTGT	ACCACACAGT	GGCTCAGCTA	900
TTCTCCCGCA	CTCTCCAGAA	CAACAGTCCC	CTCTACCAGA	ACCTCAAGGA	GAACCGCGCT	960
CCAATCTGCA	AGGACTCCTC	GTCCCTCAGG	ACCTCCTCAG	CCCTGCCTGC	CACATCCCGC	1020
CCACTGGGTG	GCGTTCTCAG	GAGCATCTCG	GTGCCTGGGC	CACCGACCCT	TCCCATGGCT	1080
GACACTTACG	CTGTGGTGCA	GAAGCGTGGC	GCTTCCGGCA	GCACAGGGCC	GGGCACGCGG	1140
GCGCCCAACA	GCACGGACAC	CCCCTCTAC	AGCCAGGTGG	CTCCACGTAT	CCAGCGGCCC	1200
GTGTACACA	CCGAAAACGC	GCAGGGGACA	ACGGCACTGG	GCCGAGTTCC	TGCGGATGAA	1260
AACCTTCCG	GGCCTGATGC	CTATGAGGAA	GTAACAGATG	GAGCGCAGAC	TGGTGGGCTA	1320
GGCTTCAACT	TGCGCATTGG	AAGACCTAAA	GGGCCACGGG	ATCCTCCAGC	GGAGTGGACA	1380
CGGGTGTAAT	GAGTGCTGTA	CCAGTTCCAG	CCTGTCACTC	AGTGGTGGCT	GGGCGACTGC	1440
AACCCCATG	CTGCTGTGTG	CTGTCTTATG	TATGAGTGGG	ACTCATGGGC	CTGAATCAAA	1500
ATAAAAGTTT	CTCAGGGTAG	AAAAAAACAA	ATAGGGACTT	TGGCCAGTGG	TTATAGCAGT	1560
CAAAGCCAGG	GGTAGGAGG	GGTAAGTGGG	GGAGGTGGTG	GATCTACTCT	GAGAAAAGTTT	1620
AGGAAAGCAC	ATCAAGAGTG	AGCATCGCCA	CTCTTCTCCC	CATACACCTA	CTGGAAAGTG	1680
CACCCAGAC	AGAGTCCTAA	CTTGACAGTG	CACCTCAGAC	AGGTCGCTAC	CTGGATGGAC	1740
ATGCTGGCCC	TACAGCTAGA	GACATGTCTA	ATTAGATCCT	CATGTAAACT	TGCAATGAGC	1800
TAGAAAGATC	TCCGTCTGGT	CAGGGAAATG	GATCACCTAG	TCAGGTAAAT	AGTGTGCCAT	1860
CCAGAAGACA	GAAGTGAAG	ATACCGTCTT	TCTCAAAATG	GAAGAAAAATA	GATCCTCAAG	1920
AATAAATGTA	TGTACAATGC	TCTACGCCCT	GATCCTGCCC	TGCCTCACTG	CCATAATGTC	1980
ACAAACAAGT	CAGGGTCTAT	ATGACAGTTG	TTCATCTAGT	CAGTCTTGAC	TGTGGCCTCT	2040
GCAGGCTCAG	ATAGTGCTTT	CTGCAGACTC	TTGGAATGCC	CGTCTTGAAC	TTGATGAAAG	2100
CTTCTACCGG	GAAGTTGTAA	ACATCATTA	AATTATTAAT	GTAGAATTCA	ATAAAGAGTG	2160
GGTCAAAAAC	TCAAAAAAAA	AAAAAAAAC	AAAAAAAAC	TCGAGAGTAC	TTCTAGAGCG	2220
GGCGGG						2226

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met	Ser	Arg	Gln	Ser	Asp	Leu	Val	Arg	Ser	Phe	Leu	Glu	Gln	Glu
1				5				10					15	
Ala	Arg	Asp	His	Arg	Lys	Gly	Ala	Ile	Leu	Ala	Arg	Glu	Phe	Ser
			20				25					30		Asp

Ile Lys Ala Arg Ser Val Ala Trp Lys Thr Glu Gly Val Cys Ser Thr
 35 40 45
 Lys Ala Gly Ser Gln Gln Gly Asn Ser Lys Lys Asn Arg Tyr Lys Asp
 50 55 60
 Val Val Pro Tyr Asp Glu Thr Arg Val Ile Leu Ser Leu Leu Gln Glu
 65 70 75 80
 Glu Gly His Gly Asp Tyr Ile Asn Ala Asn Phe Ile Arg Gly Thr Asp
 85 90 95
 Gly Ser Gln Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu
 100 105 110
 Leu Asp Phe Trp Arg Leu Val Trp Glu Phe Gly Ile Lys Val Ile Leu
 115 120 125
 Met Ala Cys Gln Glu Thr Glu Asn Gly Arg Arg Lys Cys Glu Arg Tyr
 130 135 140
 Trp Ala Gln Glu Arg Glu Pro Leu Gln Ala Gly Pro Phe Cys Ile Thr
 145 150 155 160
 Leu Thr Lys Glu Thr Ala Leu Thr Ser Asp Ile Thr Leu Arg Thr Leu
 165 170 175
 Gln Val Thr Phe Gln Lys Glu Ser Arg Pro Val His Gln Leu Gln Tyr
 180 185 190
 Met Ser Trp Pro Asp His Gly Val Pro Ser Ser Ser Asp His Ile Leu
 195 200 205
 Thr Met Val Glu Glu Ala Arg Cys Leu Gln Gly Leu Gly Pro Gly Pro
 210 215 220
 Leu Cys Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Leu Cys
 225 230 235 240
 Ala Val Asp Tyr Val Arg Gln Leu Leu Leu Thr Gln Thr Ile Pro Pro
 245 250 255
 Asn Phe Ser Leu Phe Glu Val Val Leu Glu Met Arg Lys Gln Arg Pro
 260 265 270
 Ala Ala Val Gln Thr Glu Glu Gln Tyr Arg Phe Leu Tyr His Thr Val
 275 280 285
 Ala Gln Leu Phe Ser Arg Thr Leu Gln Asn Asn Ser Pro Leu Tyr Gln
 290 295 300
 Asn Leu Lys Glu Asn Arg Ala Pro Ile Cys Lys Asp Ser Ser Ser Leu
 305 310 315 320
 Arg Thr Ser Ser Ala Leu Pro Ala Thr Ser Arg Pro Leu Gly Gly Val
 325 330 335
 Leu Arg Ser Ile Ser Val Pro Gly Pro Pro Thr Leu Pro Met Ala Asp
 340 345 350

Thr Tyr Ala Val Val Gln Lys Arg Gly Ala Ser Gly Ser Thr Gly Pro
 355 360 365
 Gly Thr Arg Ala Pro Asn Ser Thr Asp Thr Pro Ile Tyr Ser Gln Val
 370 375 380
 Ala Pro Arg Ile Gln Arg Pro Val Ser His Thr Glu Asn Ala Gln Gly
 385 390 395 400
 Thr Thr Ala Leu Gly Arg Val Pro Ala Asp Glu Asn Pro Ser Gly Pro
 405 410 415
 Asp Ala Tyr Glu Glu Val Thr Asp Gly Ala Gln Thr Gly Gly Leu Gly
 420 425 430
 Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro Pro Ala
 435 440 445
 Glu Trp Thr Arg Val
 450

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5581 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

AATTCCGGGC	GCCAGTCCCG	CTCCGCGCCG	CGCCGCTCCG	CTCCGGGCTCG	GGCTCCGGCT	60
CGCCTCGGGC	TGGGCTCGGG	CTCCGGGGGC	GGCGTCCCCG	CGCCGGGGCCC	CGGGACGCGC	120
CGACCTCCAA	CCATGGCCCC	TGCCCAGGCG	CTCGTGCTGG	CACTCACCTT	CCAGCTCTGC	180
GCGCCGGAGA	CCGAGACTCC	GGCAGCTGGC	TGCACCTTCG	AGGAGGCAAG	TGACCCAGCA	240
GTGCCCTGCG	AGTACAGCCA	GGCCCAGTAC	GATGACTTCC	AGTGGGAGCA	AGTGCGAATC	300
CACCTGGCA	CCCCGGCACC	TGCGGACCTG	CCCCACGGCT	CCTACTTGAT	GGTCAACACT	360
TCCCAGCATG	CCCCAGGCCA	GCGAGCCCAT	GTCATCTTCC	AGAGCCTGAG	CGAGAATGAT	420
ACCCACTGTG	TGCAGTTCAG	CTACTTCCTG	TACAGCCGGG	ACGGCACAGG	CGGCACCCCTG	480
CGCGTCTACG	TGCGCGTTAA	TGGGGGCCCC	CTGGCGAGTG	CTGTGTGGAA	TATGACTGGA	540
TCCCACGGCC	GTCAGTGGCA	CCAGGCTGAG	CTGGCTGTCA	GCACTTTCTG	GCCCAATGAA	600
TATCAGGTGC	TGTTTGAGGC	CCTCATCTCC	CCAGACCGCA	GGGGCTACAT	GGGCCTAGAT	660
GACATCCTGC	TTCTCAGCTA	CCCCTGCGCA	AAGGCCCCAC	ACTTCTCCCG	CCTGGGCGAC	720
GTGGAGGTCA	ACGCGGGCCA	GAACGCGTCG	TTCCAGTGCA	TGGCCGCGGG	AGAGCCCATG	780
CGCCAACGCT	TCCTCTTGCA	ACGGCAGAGC	GGGGCCCTGG	TGCCGGCCGG	GGCGTTCGGC	840
ACATCAGCCA	CCGGCTTCCT	GGCCACTTTC	CCGCTGGCTG	CCGTGAGCCG	CGCCGAGCAG	900
GACCTGTACC	GCTGTGTGTC	CCAGGCCCCG	CGCGGCGGCG	TCTCTAACTT	CCCGGAGCTC	960
ATCGTCAAGG	AGCCCCCAAC	TCCCATCGCG	CCCCACAGC	TGCTGCGTGC	TGGCCCCACC	1020
TACCTCATCA	TCCAGCTCAA	CACCAACTCC	ATCATTGGCG	ACGGGCGGAT	CGTGCGCAAG	1080
GAGATTGAGT	ACCGCATGGC	GCGCGGGCCC	TGGGCTGAGG	TGCACGCCGT	CAGCCTGCAG	1140
ACCTACAAGC	TGTGGCACCT	CGACCCCGAC	ACAGACTATG	AGATCAGCGT	GCTGCTCACG	1200
CGTCCCGGAG	ACGGCGGCAC	TGGCCGCTGG	GCCACCCCTC	ATCAGCCGCA	CCAAATGCGC	1260
AGAGCCCATG	AGGGCCCCAA	AGGCCTGGCT	TTTGCTGAGA	TCCAGGCCCC	TCAGCTGACC	1320
CTGCAGTGGG	AACCACTGGG	CTACAACGTG	ACGCGTTGCC	ACACCTATAC	TGTGTCGCTG	1380
TGCTATCACT	ACACCTGGG	CAGCAGCCAC	AACGAGACCA	TCCGAGAGTG	TGTGAAGACA	1440
GAGCAAGGTG	TCAGCCGCTA	CACCATCAAG	AACCTGTGTC	CCTATCGGAA	CGTTCACGTG	1500
AGGCTTGTCC	TACTAATCCC	TGAGGGGCGC	AAAGAGGGCA	AGGAGGTCAC	TTTCCAGACG	1560
GATGAGGATG	TGCCAGTGG	GATTGCAGCC	GAGTCCCTGA	CCTTCACTCC	ACTGGAGGAC	1620

ATGATCTTCC	TCAAGTGGGA	GGAGCCCCAG	GAGCCCAATG	GTCTCATCAC	CCAGTATGAG	1680
ATCAGCTACC	AGAGCATCGA	GTCATCAGAC	CCGGCAGTGA	ACGTGCCAGG	CCCACGACGT	1740
ACCATCTCCA	AGCTCCGCAA	TGAGACCTAC	CATGTCCTTCT	CCAACCTGCA	CCCAGGCACC	1800
ACCTACCTGT	TCTCCGTGCG	GGCCCCGACA	GGCAAAGGCT	TCGGCCAGGC	GGCACTCACT	1860
GAGATAACCA	CTAACATCTC	TGCTCCCAGC	TTTGATTATG	CCGACATGCC	GTCACCCCTG	1920
GGCGAGTCTG	AGAACACCAT	CACCGTGCTG	CTGAGGCCGG	CACAGGGCCG	CGGTGCGCCC	1980
ATCAGTGTGT	ACCAGGTGAT	TGTGGAGGAG	GAGCGGGCGC	GAGGCTGCGG	CGGGACGAGG	2040
TGGACAGGAC	TGCTTCCCAG	TGCCATTGAC	CTTCGAGGCG	GCGCTGGCCC	CAGGCTGGTG	2100
CACTACTTCG	GGGCCGAAC	GGCGGCCAGC	AGTCTACCTG	AGGCCATGCC	CTTTACCGTG	2160
GGTGACAACC	AGACCTACCG	AGGCTTCTGG	AACCCACCAC	TTGAGCCTAG	GAAGGCCTAT	2220
CTCATCTACT	TCCAGGCAGC	AAGCCACCTG	AAGGGGGAGA	CCCGGCTGAA	TTGCATCCCG	2280
ATTGCCAGGA	AAGCTGCCTG	CAAGGAAAGC	AAGCGGCCCC	TGGAGGTGTC	CCAGAGATCG	2340
GAGGAGATGG	GGCTTATCCT	GGGCATCTGT	GCAGGGGGGC	TTGCTGTCCT	CATCCTTCTC	2400
CTGGGTGCCA	TCATTGTGAT	CATCCGCAAA	GGGAAGCCGG	TGAACATGAC	CAAGGCCACC	2460
GTCAACTACC	GCCAGGAGAA	GACACACATG	ATCAGCGCCG	TGGACCGCAG	CTTCACAGAC	2520
CAGAGCACCC	TGCAGGAGGA	CGAGCGGCTG	GGCCTGTCC	TCATGGACAC	CCATGGCTAC	2580
AGCACCCGGG	GAGACCAGCG	CAGCGGTGGG	GTCCTGAGG	CCAGCAGCCT	CCTGGGGGGG	2640
TCCCCGAGGC	GTCCCTGTGG	CCGGAAGGGC	TCCCATACC	ACACGGGGCA	GCTGCACCCT	2700
GCGGTGCGTG	TCGCAGACCT	TCTGCAGCAC	ATCAACCAGA	TGAAGACGGC	CGAGGGTTAC	2760
GGCTTCAAGC	AGGAGTATGA	GAGCTTCTTT	GAAGGCTGGG	ACGCCACAAA	GAAGAAAAGAC	2820
AAGGTCAAGG	GCAGCCGGCA	GGAGCCAATG	CCTGCCATATG	ATCGGCACCG	AGTGAAACTG	2880
CACCCGATGC	TGGGAGACCC	CAATGCCGAC	TACATTAATG	CCAACTACAT	AGATGGTTAC	2940
CACAGGTCAA	ACCACCTCAT	AGCCACTCAA	GGGCCGAAGC	CTGAGATGGT	CTATGACTTC	3000
TGGCGTATGG	TGTGGCAGGA	GCACTGTTCC	AGCATCGTCA	TGATACCCAA	GCTGGTCGAG	3060
GTGGGCAGGG	TGAAATGCTC	ACGGTACTGG	CCGGAGGACT	CAGACACCTA	CGGGGACATC	3120
AAGATTATGC	TGGTGAAGAC	AGAGACCCTG	GCTGAGTATG	TCGTGCGCAC	TTTTGCCCTG	3180
GAGCGGAGAG	GCTACTCTGC	CCGGCAGCAG	GTCCGCCAGT	CCCACTTCAC	AGCGTGGCCA	3240
GAGCATGGCG	TCCCCTACCA	TGCCACGGGG	CTGCTGGCTT	TCATCCGGCG	GGTGAAGGCC	3300
TCCACCCAC	CTGATGCCCG	GCCCATGTG	ATCCACTGCA	GCGCGGGCAC	CGGCCGCACA	3360
CGTTGCTATA	TCGTCTGGA	TGTGATGCTG	GACATGGCAG	AGTGTGAGGG	CGTCCGTGGAC	3420
ATTTACAAC	GTGTGAAGAC	TCTCTGCTCC	CGGCGTGTCA	ACATGATCCA	GACTGAGGAG	3480
CAGTACATCT	TCATTTCATG	TGCAATCCTG	GAGGCCCTGCC	TGTGTGGGGA	GACCACCATC	3540
CCTGTCAAGT	AGTTCAAGGC	CACCTACAAG	GAGATGATCC	GCATTGATCC	TCAGAGTAAT	3600
TCCTCCAGC	TGCGGGAAGA	GTTCCAGACG	CTGAACTCGG	TCACCCCGCC	GCTGGACGTG	3660
GAGGAGTACA	GCATCGCCCT	GTTGCCCCGG	AACCGCGACA	AGAACCGCAG	CATGGACGTC	3720
CTGCCGCCCC	ACCGCTGCCT	GCCCTTCCCT	ATCTCCACTG	ATGGGGACTC	CAACAACTAC	3780
ATTAATGCAG	CCCTGACTGA	CAGCTACACA	CGGAGGTCGG	CCTTCATGGT	GACCCTGCAC	3840
CCGCTGCAGA	GCACCACGCC	CGACTTCTGG	CGGCTGGTCT	ACGATTACGG	GTGCACCTCC	3900
ATCGTTCATG	TCAACCAGCT	GAACCAGTCC	AACTCCGCCT	GGCCCTGCCT	GCACTACTGG	3960
CCAGAGCCAG	GCCGGCAGCA	ATATGGCCTC	ATGGAGGTGG	AGTTTATGTC	GGGCACAGCT	4020
GATGAAGACT	TAGTGGCTCG	AGTCTTCCGG	GTGCAAAACA	TCTCTCGGTT	GCAGGAGGGA	4080
GACCTGCTGG	TGCGGCACCT	CCAGTTCCCTG	CGCTGGTCTG	CATACCGGGA	CACACCTGAC	4140
TCCAAGAAGG	CCTTCTTGCA	CCTGCTGGCT	GAGGTGGACA	AGTGGCAGGC	CGAGAGTGGG	4200
GATGGGCGCA	CCATCGTGCA	CTGCCTAAAC	GGGGGAGGAC	GCAGCGGCAC	CTTCTGCGCC	4260
TGCGCCACGG	TCCTGGAGAT	GATCCGCTGC	CACAACCTGG	TGGACGTTTT	CTTTGCTGCC	4320
CAAACCTCC	GGAACACAA	ACCCAACATG	GTGGAGACCA	TGGATCAGTA	CCACTTTTGC	4380
TACGATGTGG	CCCTGGAGTA	CTTGGAGGGG	CTGGAGTCAA	GATAGCGGGG	CCCTGGCCTG	4440
GGGCACCCAC	TGCACACTCA	GGGCCAGACC	CACCATCCTG	GACTGGCGAG	GAAGATCAGT	4500
GCCTCCTGCT	CTGCCCCAAC	ACACTCCCAT	GGGGCAAGCA	CTGGAGTGGA	TGCTGGGCTA	4560
TCTTGCTCCC	CCTTCCACTG	TGGGCAGGGC	CTTTCGCTTG	TCCCATGGGC	GGGTGGTGGG	4620
CCAAGGAGGA	GCTTAGCAAG	TCTGCACCCC	ACCCCCACCT	CCATAGGGTC	CTGCAGGCCT	4680
GTGCTGAGAG	GCCTGGTGCT	GCCTGGCAGA	GTGACAAAGG	CTCAGGACGG	CTGGCTCTGG	4740
GGGACTCAGG	CCAAGGGGGT	TGGCAGGATC	CTGGGTTTGG	GGAGGGATGA	GTGAGGCCCT	4800
GCAGAGAGCA	TCCCAGGCCA	AGGTTCCCAT	TCAGCCTGCC	CCCTCTGCAT	GTGGGTAGAG	4860
GATGTACTGG	GACTTGGCAT	TTAGGATTCC	ATCTGGGGGA	CCCCCTGAAG	GTCCCCCCCCA	4920
AGCAGGTCTC	AATTCTGATA	GCCAGTGGGG	CACACTGACT	GTCTCCCCCA	GGGGAACCTGC	4980
AGCGCCCTCC	TCCCCACTGC	CCCCCTCCAGC	CCCTGAGATA	TTTTTGCTCAC	TATCCCTCCC	5040
CACCTGCTTC	CCTGATATGT	GCTCTGACTT	CCCTGAACCA	GGATCTGCCT	ATTACTGCTG	5100
TCCCATGGGG	GCTCTCTTCC	CGCTCTGACC	CCTGTCTGCA	GAATGAAGTC	ACCTCGCCCC	5160
CCTCTTCCTT	TAATCTTCAG	GCCTCACTGG	CTGTCTCTGC	TCAGCTTGGG	CCAGTGACAA	5220
TCTGCAAGGC	TGAACAACAG	CCCCTGGGGT	TGAGGCCCTT	GTGGCTCCTG	GTCAGGCTGC	5280
CCGTTGTGGG	GAGGGGCAGT	GTTAGAGCAG	GGCTGGTCAT	ACCCTCTGGA	GTTTCAGAGCA	5340

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AGAGGTAGGA CCAGTGCTTT TTTGTTTCTT TTGTTATTTT TGGTTGGGTG GGTGGGAAGG 5400
TCTCTTTAAA ATGGGGCAGG CCACACCCCC ATTCCGTGCC TCAATTTCCC CATCTGTAAA 5460
CTGTAGATAT GACTACTGAC CTACCTCGCA GGGGGCTGTG GGGAGGCATA AGCTGATGTT 5520
TGTAAGCGC TTTGTAAATA AACGTGCTCT CTGAATGCCA AAAAAAAAAA AACAAAAAAAAA 5580
A 5581

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(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH:      1430 amino acids
(B) TYPE:        amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY:    linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

Met Ala Arg Ala Gln Ala Leu Val Leu Ala Leu Thr Phe Gln Leu Cys
 1           5           10           15
Ala Pro Glu Thr Glu Thr Pro Ala Ala Gly Cys Thr Phe Glu Glu Ala
      20           25           30
Ser Asp Pro Ala Val Pro Cys Glu Tyr Ser Gln Ala Gln Tyr Asp Asp
      35           40           45
Phe Gln Trp Glu Gln Val Arg Ile His Pro Gly Thr Arg Ala Pro Ala
      50           55           60
Asp Leu Pro His Gly Ser Tyr Leu Met Val Asn Thr Ser Gln His Ala
      65           70           75           80
Pro Gly Gln Arg Ala His Val Ile Phe Gln Ser Leu Ser Glu Asn Asp
      85           90           95
Thr His Cys Val Gln Phe Ser Tyr Phe Leu Tyr Ser Arg Asp Gly Thr
      100          105          110
Gly Gly Thr Leu Arg Val Tyr Val Arg Val Asn Gly Gly Pro Leu Ala
      115          120          125
Ser Ala Val Trp Asn Met Thr Gly Ser His Gly Arg Gln Trp His Gln
      130          135          140
Ala Glu Leu Ala Val Ser Thr Phe Trp Pro Asn Glu Tyr Gln Val Leu
      145          150          155          160
Phe Glu Ala Leu Ile Ser Pro Asp Arg Arg Gly Tyr Met Gly Leu Asp
      165          170          175
Asp Ile Leu Leu Leu Ser Tyr Pro Cys Ala Lys Ala Pro His Phe Ser
      180          185          190
Arg Leu Gly Asp Val Glu Val Asn Ala Gly Gln Asn Ala Ser Phe Gln
      195          200          205
Cys Met Ala Ala Gly Glu Pro Met Arg Gln Arg Phe Leu Leu Gln Arg
      210          215          220

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Gln Ser Gly Ala Leu Val Pro Ala Gly Ala Phe Gly Thr Ser Ala Thr
 225 230 235 240
 Gly Phe Leu Ala Thr Phe Pro Leu Ala Ala Val Ser Arg Ala Glu Gln
 245 250 255
 Asp Leu Tyr Arg Cys Val Ser Gln Ala Pro Arg Gly Gly Val Ser Asn
 260 265 270
 Phe Pro Glu Leu Ile Val Lys Glu Pro Pro Thr Pro Ile Ala Pro Pro
 275 280 285
 Gln Leu Leu Arg Ala Gly Pro Thr Tyr Leu Ile Ile Gln Leu Asn Thr
 290 295 300
 Asn Ser Ile Ile Gly Asp Gly Pro Ile Val Arg Lys Glu Ile Glu Tyr
 305 310 315 320
 Arg Met Ala Arg Gly Pro Trp Ala Glu Val His Ala Val Ser Leu Gln
 325 330 335
 Thr Tyr Lys Leu Trp His Leu Asp Pro Asp Thr Asp Tyr Glu Ile Ser
 340 345 350
 Val Leu Leu Thr Arg Pro Gly Asp Gly Gly Thr Gly Arg Trp Ala Thr
 355 360 365
 Pro His Gln Pro His Gln Met Arg Arg Ala His Glu Gly Pro Lys Gly
 370 375 380
 Leu Ala Phe Ala Glu Ile Gln Ala Arg Gln Leu Thr Leu Gln Trp Glu
 385 390 395 400
 Pro Leu Gly Tyr Asn Val Thr Arg Cys His Thr Tyr Thr Val Ser Leu
 405 410 415
 Cys Tyr His Tyr Thr Leu Gly Ser Ser His Asn Gln Thr Ile Arg Glu
 420 425 430
 Cys Val Lys Thr Glu Gln Gly Val Ser Arg Tyr Thr Ile Lys Asn Leu
 435 440 445
 Leu Pro Tyr Arg Asn Val His Val Arg Leu Val Leu Thr Asn Pro Glu
 450 455 460
 Gly Arg Lys Glu Gly Lys Glu Val Thr Phe Gln Thr Asp Glu Asp Val
 465 470 475 480
 Pro Ser Gly Ile Ala Ala Glu Ser Leu Thr Phe Thr Pro Leu Glu Asp
 485 490 495
 Met Ile Phe Leu Lys Trp Glu Glu Pro Gln Glu Pro Asn Gly Leu Ile
 500 505 510
 Thr Gln Tyr Glu Ile Ser Tyr Gln Ser Ile Glu Ser Ser Asp Pro Ala
 515 520 525
 Val Asn Val Pro Gly Pro Arg Arg Thr Ile Ser Lys Leu Arg Asn Glu
 530 535 540

Thr Tyr His Val Phe Ser Asn Leu His Pro Gly Thr Thr Tyr Leu Phe
 545 550 555 560
 Ser Val Arg Ala Arg Thr Gly Lys Gly Phe Gly Gln Ala Ala Leu Thr
 565 570 575
 Glu Ile Thr Thr Asn Ile Ser Ala Pro Ser Phe Asp Tyr Ala Asp Met
 580 585 590
 Pro Ser Pro Leu Gly Glu Ser Glu Asn Thr Ile Thr Val Leu Leu Arg
 595 600 605
 Pro Ala Gln Gly Arg Gly Ala Pro Ile Ser Val Tyr Gln Val Ile Val
 610 615 620
 Glu Glu Glu Arg Ala Arg Gly Cys Gly Gly Thr Arg Trp Thr Gly Leu
 625 630 635 640
 Leu Pro Ser Ala Ile Asp Leu Arg Gly Gly Ala Gly Pro Arg Leu Val
 645 650 655
 His Tyr Phe Gly Ala Glu Leu Ala Ala Ser Ser Leu Pro Glu Ala Met
 660 665 670
 Pro Phe Thr Val Gly Asp Asn Gln Thr Tyr Arg Gly Phe Trp Asn Pro
 675 680 685
 Pro Leu Glu Pro Arg Lys Ala Tyr Leu Ile Tyr Phe Gln Ala Ala Ser
 690 695 700
 His Leu Lys Gly Glu Thr Arg Leu Asn Cys Ile Arg Ile Ala Arg Lys
 705 710 715 720
 Ala Ala Cys Lys Glu Ser Lys Arg Pro Leu Glu Val Ser Gln Arg Ser
 725 730 735
 Glu Glu Met Gly Leu Ile Leu Gly Ile Cys Ala Gly Gly Leu Ala Val
 740 745 750
 Leu Ile Leu Leu Leu Gly Ala Ile Ile Val Ile Ile Arg Lys Gly Lys
 755 760 765
 Pro Val Asn Met Thr Lys Ala Thr Val Asn Tyr Arg Gln Glu Lys Thr
 770 775 780
 His Met Ile Ser Ala Val Asp Arg Ser Phe Thr Asp Gln Ser Thr Leu
 785 790 795 800
 Gln Glu Asp Glu Arg Leu Gly Leu Ser Phe Met Asp Thr His Gly Tyr
 805 810 815
 Ser Thr Arg Gly Asp Gln Arg Ser Gly Gly Val Thr Glu Ala Ser Ser
 820 825 830
 Leu Leu Gly Gly Ser Pro Arg Arg Pro Cys Gly Arg Lys Gly Ser Pro
 835 840 845
 Tyr His Thr Gly Gln Leu His Pro Ala Val Arg Val Ala Asp Leu Leu
 850 855 860
 Gln His Ile Asn Gln Met Lys Thr Ala Glu Gly Tyr Gly Phe Lys Gln
 865 870 875 880

SD-88184.1

Arg Cys Leu Pro Phe Leu Ile Ser Thr Asp Gly Asp Ser Asn Asn Tyr
 1205 1210 1215
 Ile Asn Ala Ala Leu Thr Asp Ser Tyr Thr Arg Arg Ser Ala Phe Met
 1220 1225 1230
 Val Thr Leu His Pro Leu Gln Ser Thr Thr Pro Asp Phe Trp Arg Leu
 1235 1240 1245
 Val Tyr Asp Tyr Gly Cys Thr Ser Ile Val Met Leu Asn Gln Leu Asn
 1250 1255 1260
 Gln Ser Asn Ser Ala Trp Pro Cys Leu Gln Tyr Trp Pro Glu Pro Gly
 1265 1270 1275 1280
 Arg Gln Gln Tyr Gly Leu Met Glu Val Glu Phe Met Ser Gly Thr Ala
 1285 1290 1295
 Asp Glu Asp Leu Val Ala Arg Val Phe Arg Val Gln Asn Ile Ser Arg
 1300 1305 1310
 Leu Gln Glu Gly Asp Leu Leu Val Arg His Phe Gln Phe Leu Arg Trp
 1315 1320 1325
 Ser Ala Tyr Arg Asp Thr Pro Asp Ser Lys Lys Ala Phe Leu His Leu
 1330 1335 1340
 Leu Ala Glu Val Asp Lys Trp Gln Ala Glu Ser Gly Asp Gly Arg Thr
 1345 1350 1355 1360
 Ile Val His Cys Leu Asn Gly Gly Gly Arg Ser Gly Thr Phe Cys Ala
 1365 1370 1375
 Cys Ala Thr Val Leu Glu Met Ile Arg Cys His Asn Leu Val Asp Val
 1380 1385 1390
 Phe Phe Ala Ala Gln Thr Leu Arg Asn Tyr Lys Pro Asn Met Val Glu
 1395 1400 1405
 Thr Met Asp Gln Tyr His Phe Cys Tyr Asp Val Ala Leu Glu Tyr Leu
 1410 1415 1420
 Glu Gly Leu Glu Ser Arg
 1425 1430

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GAATTCGGCA CGAGCGGGCT GGACCTTGCT CGCCCGCGGC GCCATGAGCC GCAGCCTGGA	60
CTCGGCGCCG AGCTTCCTGG AGCGGCTGGA AGCGCGGGGC GGCCGGGAGG GGGCAGTCCT	120
CGCCGGCGAG TTCAGCGACA TCCAGGCCTG CTCGGCCGCC TGAAGGCTG ACGGCGTGTG	180

CTCCACCGTG	GCCGGCAGTC	GGCCAGAGAA	CGTGAGGAAG	AACCGCTACA	AAGACGTGCT	240
GCCTTATGAT	CAGACGCGAG	TAATCCTCTC	CCTGCTCCAG	GAAGAGGGAC	ACAGCGACTA	300
CATTAATGGC	AACCTTCATCC	GGGGCGTGGA	TGGAAGCCTG	GCCTACATTG	CCACGCAAGG	360
ACCCTTGCTT	CACACCCTGC	TAGACTTCTG	GAGACTGGTC	TGGGAGTTTG	GGGTCAAGGT	420
GATCCTGATG	GCCTGTGAG	AGATAGAGAA	TGGGCGGAAA	AGGTGTGAGC	GGTACTGGGC	480
CCAGGAGCAG	GAGCCACTGC	AGACTGGGCT	TTTCTGCATC	ACTCTGATAA	AGGAGAAGTG	540
GCTGAATGAG	GACATCATGC	TCAGGACCTT	CAAGGTCACA	TTCCAGAAGG	AGTCCCCTTC	600
TGTGTACCAG	CTACAGTATA	TGTCTGGGCC	AGACCGTGGG	GTCCCCAGCA	GTCCTGACCA	660
CATGCTCGCC	ATGGTGGAGG	AAGCCCGTCG	CCTCCAGGGA	TCTGGCCCTG	AACCCCTCTG	720
TGTCCACTGC	AGTGCGGGTT	GTGGGCGAAC	AGGCGTCTTG	TGCACCGTGG	ATTATGTGAG	780
GCAGCTGCTC	CTGACCCAGA	TGATCCCACC	TGACTTCAGT	CTCTTTGATG	TGGTCCCTAA	840
GATGAGGAAG	CAGCGGCCCTG	CGGCCGTGCA	GACAGAGGAG	CAGTACAGGT	TCCTGTACCA	900
CACGGTGGCT	CAGATGTTCT	GCTCCACACT	CCAGAATGCC	AGCCCCCACT	ACCAGAACAT	960
CAAAGAGAAT	TGTGCCCCAC	TCTACGACGA	TGCCCTCTTC	CTCCGGACTC	CCCAGGCACT	1020
TCTCGCCATA	CCCCGCCCAC	CAGGAGGGGT	CCTCAGGAGC	ATCTCTGTGC	CCGGGTCCCC	1080
GGGCCACGCC	ATGGCTGACA	CCTACGCGGA	GGAGCAGAAG	CGCGGGGCTC	CAGCGGGCGC	1140
CGGGAGTGGG	ACGCAGACGG	GGACGGGGAC	GGGGGCGCGC	AGGGCGGAGG	AGGCGCCGCT	1200
CTACAGCAAG	GTGACGCGC	GCGCCAGCG	ACCGGGGCG	CACGCGGAGG	ACGCGAGGGG	1260
GACGCTGCCT	GGCCGCGTTC	CTGCTGACCA	AAGTCTTGCC	GGATCTGGCG	CCTACGAGGA	1320
CGTGGCGGGT	GGAGCTCAGA	CCGGTGGGCT	AGGTTTCAAC	CTGCGCATTG	GGAGGCCGAA	1380
GGGTCCCCGG	GACCCGCTTG	CTGAGTGGAC	CCGGGTGTAA	GTCTAACGCC	AGTTCCTGCC	1440
TGTTGCCTCT	TGTGAGCTCG	GAATGCTGAT	GCCCCGGTGC	TGCTGAGCGC	CGTGCCGAGA	1500
ATGGAAACAG	TGGGCCTGGA	TCAAAGTTAA	AGTTTCTCAG	GGTGGGAAAT	GTGGGGGCTT	1560
TGCCCCAATGA	CTGTAGCATT	CAAGGCTTGA	GGCTGGAGGA	GGTAGCTAGG	GTATAGTGGC	1620
TGGTGAGGCT	GCACAGAGCA	GATTCAAGAA	AGAAGATCAG	GAAGGGGCAT	GACCCCTGAG	1680
TTATGAAGGG	GAGAAGGGAC	AGATGAGCTT	CCGGAGACTG	CTCTCCTCAC	CACACAGCAC	1740
TAGTCCATCC	TCAGCACCTG	AGCCTCCCTC	ACTTGGACAC	TCAGGGGACC	ACACAGAGAA	1800
GTGGATGGAC	ACTTCGCCAT	CCAGGCAGAA	CTAAGCCAGG	CATAACCACA	GCCAAGCAGA	1860
TTAACCCAG	GCAGACCGAT	AAAAAGACCT	CCAGATAGGC	AGACAGACAG	ATGGACCACC	1920
AACCTGGACA	GACAGCCAAA	GCTTCAGAGA	TACAGTCCAC	AGGTGGACAA	AGGATCCCCC	1980
AGCCAGAGAG	AGAGAGACCA	GCCAACAGCT	TGATAGACCA	GTGCAGCCAG	AGAGACCACC	2040
AAACACAGCC	CCCAAAAGAC	AGACATCTCT	GCTAGCTGGA	CAGCCAGGTG	GACCCCTTAA	2100
GTTAGTCAGA	TTACTAGACA	GATATAAACA	GATCCCCTGC	TGAACAGATA	TACAGAGTTC	2160
TCAGACCCCA	CTCCCTCAGG	TGGGCTGGCT	GGCTGACAGA	CCTTCTGGCC	AGACAGACTC	2220
CTAACCAACC	AGATGGACTG	CCAGACAGGC	AGACATCAGT	CCACATGGAA	TCCTGACATC	2280
CCAGCCAGCC	GGCCAGACTC	TCATCTTGAT	GTCTTGATGG	ATGGACCCCA	GCTAGTCAGA	2340
CATGATCCTC	CAGATTGACA	GACAAGTCCC	CCAAATGAGT	ACACATCTCC	AGCTATTTCAG	2400
ACAGATGGAG	CCCCAGCAAA	TCAGGACCTA	TCTAGGCAGA	CCCCAGCCAG	ACCCCGGCCA	2460
GACAGACTCC	CAACCAGACT	GACCCCTTGC	TGTTACACAC	GCCTGCCGAG	TAGCTGGGAC	2520
TACAGGTCTA	ATTTTTTTTT	TTTTTAAGAA	ATGAGTTTTT	GCCATGTTGC	CCAGACTGGT	2580
CTTGAACCTC	CAACCTCAAG	CAATCCTCCT	GCCTCAGCCT	CCCAAAGTGC	TGAGATTACA	2640
GGTGTGAGCC	ACCAGGCTCA	GCCCCCTAAG	ATTTGAAACA	CTTTAAATGG	CCCATGGTAG	2700
GGTTCCTGCT	AGGATAAAAC	ATTAAGTGGC	TGTTAAAGA	AATAAAAGGA	GGACACGTCT	2760
CTGTGCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		2810

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met Ser Arg Ser Leu Asp Ser Ala Pro Ser Phe Leu Glu Arg Leu Glu
 1 5 10 15
 Ala Arg Gly Gly Arg Glu Gly Ala Val Leu Ala Gly Glu Phe Ser Asp
 20 25 30
 Ile Gln Ala Cys Ser Ala Ala Trp Lys Ala Asp Gly Val Cys Ser Thr
 35 40 45
 Val Ala Gly Ser Arg Pro Glu Asn Val Arg Lys Asn Arg Tyr Lys Asp
 50 55 60
 Val Leu Pro Tyr Asp Gln Thr Arg Val Ile Leu Ser Leu Leu Gln Glu
 65 70 75 80
 Glu Gly His Ser Asp Tyr Ile Asn Gly Asn Phe Ile Arg Gly Val Asp
 85 90 95
 Gly Ser Leu Ala Tyr Ile Ala Thr Gln Gly Pro Leu Pro His Thr Leu
 100 105 110
 Leu Asp Phe Trp Arg Leu Val Trp Glu Phe Gly Val Lys Val Ile Leu
 115 120 125
 Met Ala Cys Arg Glu Ile Glu Asn Gly Arg Lys Arg Cys Glu Arg Tyr
 130 135 140
 Trp Ala Gln Glu Gln Glu Pro Leu Gln Thr Gly Leu Phe Cys Ile Thr
 145 150 155 160
 Leu Ile Lys Glu Lys Trp Leu Asn Glu Asp Ile Met Leu Arg Thr Leu
 165 170 175
 Lys Val Thr Phe Gln Lys Glu Ser Arg Ser Val Tyr Gln Leu Gln Tyr
 180 185 190
 Met Ser Trp Pro Asp Arg Gly Val Pro Ser Ser Pro Asp His Met Leu
 195 200 205
 Ala Met Val Glu Glu Ala Arg Arg Leu Gln Gly Ser Gly Pro Glu Pro
 210 215 220
 Leu Cys Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Leu Cys
 225 230 235 240
 Thr Val Asp Tyr Val Arg Gln Leu Leu Leu Thr Gln Met Ile Pro Pro
 245 250 255
 Asp Phe Ser Leu Phe Asp Val Val Leu Lys Met Arg Lys Gln Arg Pro
 260 265 270
 Ala Ala Val Gln Thr Glu Glu Gln Tyr Arg Phe Leu Tyr His Thr Val
 275 280 285
 Ala Gln Met Phe Cys Ser Thr Leu Gln Asn Ala Ser Pro His Tyr Gln
 290 295 300
 Asn Ile Lys Glu Asn Cys Ala Pro Leu Tyr Asp Asp Ala Leu Phe Leu
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Met 1	Glu	Pro	Ala	Gly 5	Pro	Ala	Pro	Gly	Arg 10	Leu	Gly	Pro	Leu	Leu 15	Cys
Leu	Leu	Leu	Ala 20	Ala	Ser	Cys	Ala	Trp 25	Ser	Gly	Val	Ala	Gly 30	Glu	Glu
Glu	Leu	Gln 35	Val	Ile	Gln	Pro	Asp 40	Lys	Ser	Val	Ser	Val 45	Ala	Ala	Gly
Glu 50	Ser	Ala	Ile	Leu	His	Cys 55	Thr	Val	Thr	Ser	Leu 60	Ile	Pro	Val	Gly
Pro 65	Ile	Gln	Trp	Phe 70	Arg	Gly	Ala	Gly	Pro	Ala 75	Arg	Glu	Leu	Ile 80	Tyr
Asn	Gln	Lys	Glu	Gly 85	His	Phe	Pro	Arg	Val 90	Thr	Thr	Val	Ser	Glu 95	Ser
Thr	Lys	Arg	Glu 100	Asn	Met	Asp	Phe	Ser 105	Ile	Ser	Ile	Ser	Asn 110	Ile	Thr

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 115 120 125
 Pro Asp Thr Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
 130 135 140
 Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Ala Arg Ala Thr
 145 150 155 160
 Pro Gln His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
 165 170 175
 Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
 180 185 190
 Phe Gln Thr Asn Val Asp Pro Val Gly Glu Ser Val Ser Tyr Ser Ile
 195 200 205
 His Ser Thr Ala Lys Val Val Leu Thr Arg Glu Asp Val His Ser Gln
 210 215 220
 Val Ile Cys Glu Val Ala His Val Thr Leu Gln Gly Asp Pro Leu Arg
 225 230 235 240
 Gly Thr Ala Asn Leu Ser Glu Thr Ile Arg Val Pro Pro Thr Leu Glu
 245 250 255
 Val Thr Gln Gln Pro Val Arg Ala Glu Asn Gln Val Asn Val Thr Cys
 260 265 270
 Gln Val Arg Lys Phe Tyr Pro Gln Arg Leu Gln Leu Thr Trp Leu Glu
 275 280 285
 Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Val Thr Glu Asn
 290 295 300
 Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Val Ser
 305 310 315 320
 Ala His Arg Asp Asp Val Lys Leu Thr Cys Gln Val Glu His Asp Gly
 325 330 335
 Gln Pro Ala Val Ser Lys Ser His Asp Leu Lys Val Ser Ala His Pro
 340 345 350
 Lys Glu Gln Gly Ser Asn Thr Ala Ala Glu Asn Thr Gly Ser Asn Glu
 355 360 365
 Arg Asn Ile Tyr Ile Val Val Gly Val Val Cys Thr Leu Leu Val Ala
 370 375 380
 Leu Leu Met Ala Ala Leu Tyr Leu Val Arg Ile Arg Gln Lys Lys Ala
 385 390 395 400
 Gln Gly Ser Thr Ser Ser Thr Arg Leu His Glu Pro Glu Lys Asn Ala
 405 410 415
 Arg Glu Ile Thr Gln Asp Thr Asn Asp Ile Thr Tyr Ala Asp Leu Asn
 420 425 430

Leu Pro Lys Gly Lys Lys Pro Ala Pro Gln Ala Ala Glu Pro Asn Asn
 435 440 445
 His Thr Glu Tyr Ala Ser Ile Gln Thr Ser Pro Gln Pro Ala Ser Glu
 450 455 460
 Asp Thr Leu Thr Tyr Ala Asp Leu Asp Met Val His Leu Asn Arg Thr
 465 470 475 480
 Pro Lys Gln Pro Ala Pro Lys Pro Glu Pro Ser Phe Ser Glu Tyr Ala
 485 490 495
 Ser Val Gln Val Pro Arg Lys
 500

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Met Pro Val Pro Ala Ser Trp Pro His Leu Pro Ser Pro Phe Leu Leu
 1 5 10 15
 Met Thr Leu Leu Leu Gly Arg Leu Thr Gly Val Ala Gly Glu Asp Glu
 20 25 30
 Leu Gln Val Ile Gln Pro Glu Lys Ser Val Ser Val Ala Ala Gly Glu
 35 40 45
 Ser Ala Thr Leu Arg Cys Ala Met Thr Ser Leu Ile Pro Val Gly Pro
 50 55 60
 Ile Met Trp Phe Arg Gly Ala Gly Ala Gly Arg Glu Leu Ile Tyr Asn
 65 70 75 80
 Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Leu Thr
 85 90 95
 Lys Arg Asn Asn Leu Asn Phe Ser Ile Ser Ile Ser Asn Ile Thr Pro
 100 105 110
 Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro
 115 120 125
 Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg
 130 135 140
 Ala Lys Pro Ser Ala Pro Val Val Ser Gly Pro Ala Val Arg Ala Thr
 145 150 155 160
 Pro Glu His Thr Val Ser Phe Thr Cys Glu Ser His Gly Phe Ser Pro
 165 170 175

Arg Asp Ile Thr Leu Lys Trp Phe Lys Asn Gly Asn Glu Leu Ser Asp
 180 185 190
 Phe Gln Thr Asn Val Asp Pro Ala Gly Asp Ser Val Ser Tyr Ser Ile
 195 200 205
 His Ser Thr Ala Arg Val Val Leu Thr Arg Gly Asp Val His Ser Gln
 210 215 220
 Val Ile Cys Glu Met Ala His Ile Thr Leu Gln Gly Asp Pro Leu Arg
 225 230 235 240
 Gly Thr Ala Asn Leu Ser Glu Ala Ile Arg Val Pro Pro Thr Leu Glu
 245 250 255
 Val Thr Gln Gln Pro Met Arg Ala Glu Asn Gln Ala Asn Val Thr Cys
 260 265 270
 Gln Val Ser Asn Phe Tyr Pro Arg Gly Leu Gln Leu Thr Trp Leu Glu
 275 280 285
 Asn Gly Asn Val Ser Arg Thr Glu Thr Ala Ser Thr Leu Thr Glu Asn
 290 295 300
 Lys Asp Gly Thr Tyr Asn Trp Met Ser Trp Leu Leu Val Asn Thr Cys
 305 310 315 320
 Ala His Arg Asp Asp Val Val Leu Thr Cys Gln Val Glu His Asp Gly
 325 330 335
 Gln Gln Ala Val Ser Lys Ser Tyr Ala Leu Glu Ile Ser Ala His Gln
 340 345 350
 Lys Glu His Gly Ser Asp Ile Thr His Glu Pro Ala Leu Ala Pro Thr
 355 360 365
 Ala Pro Leu Leu Val Ala Leu Leu Leu Gly Pro Lys Leu Leu Leu Val
 370 375 380
 Val Gly Val Ser Ala Ile Tyr Ile Cys Trp Lys Gln Lys Ala
 385 390 395